SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Opperman, Hermann
Ozkaynak, Engin
Rueger, David C.
Kuberasampath, Thangavel

(ii) TITLE OF INVENTION: Osteogenic Proteins

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:
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(B) STREET: 60 State Street
(C) CITY: Boston
(D) STATE: Massachusetts
(E) COUNTRY: U.S.A.
(F) ZIP: 02109

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette, 3.5 inch, 720kb storage
(B) COMPUTER: IBM XT
(C) OPERATING SYSTEM: DOS 3.30
(D) SOFTWARE: Word Perfect 5.0

(vi) CURRENT APPLICATION DATA:
(B) FILING DATE: 18-Oct-90

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 569,920
(B) FILING DATE: 20-Aug-90
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(D) FILING DATE: 23-Feb-89
(E) APPLICATION NUMBER: US 422,699
(F) FILING DATE: 17-Oct-89

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala	Ala	Arg	Pro	Leu	Lys	Arg	Gln
Pro	Lys	Lys	Thr	Asn	Glu	Leu	Pro	His
Pro	Asn	Lys	Leu	Pro	Gly	Ile	Phe	Asp
Asp	Gly	His	Gly	Ser	Arg	Gly	Arg	Glu
Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
Arg	Phe	Arg	Asp	Leu	Gly	Trp	Leu	Asp
Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
Val	His	Leu	Met	Lys	Pro	Asp	Val	Val
Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr

```
Asp  Ser  Ser  Asn  Asn  Val  Ile  Leu  Arg
          120                      125

Lys  His  Arg  Asn  Met  Val  Val  Lys  Ala
               130                      135

Cys  Gly  Cys  His.
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1930 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Bovinae

(F) TISSUE TYPE: bone

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: mouse embryo

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
GGAATTCCGC TGCCAGGCAC AGGTGCGCCG TCTGGTCCTC     40
CCCGTCTGGC GTCAGCCGAG CCCGACCAGC TACCAGTGGA     80
TGCGCGCCGG CTGAAAGTCC GAG ATG GCT ATG CGT      115
                          Met Ala Met Arg
                            1

CCC GGG CCA CTC TGG CTA TTG GGC CTT GCT CTG    148
Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu
  5                  10                  15

TGC GCG CTG GGA GGC GGC CAC GGT CCC GGT CCC    181
Cys Ala Leu Gly Gly Gly His Gly Pro Gly Pro
                 20                  25
```

```
CCG CAC ACC TGT CCC CAG CGT CGC CTG GGA GCG   214
Pro His Thr Cys Pro Gln Arg Arg Leu Gly Ala
            30                  35

CGC GAC CGG GAC ATG CAG CGT GAA ATC CTG CCG   247
Arg Asp Arg Asp Met Gln Arg Glu Ile Leu Pro
        40                  45

GTG CTC GGG CTA CCG GGA CGC CCC GAC CCC GTG   280
Val Leu Gly Leu Pro Gly Arg Pro Asp Pro Val
    50                  55

CAC AAC CCG CCG CTG CCC GGC ACG CAG CGT GCG   313
His Asn Pro Pro Leu Pro Gly Thr Gln Arg Ala
60                  65                  70

CCC CTC TTC ATG TTG GAC CTA TAC CAC GCC ATG   346
Pro Leu Phe Met Leu Asp Leu Tyr His Ala Met
                75                  80

ACC GAT GAC GAC GAC GGC GGG CCA CCA CAG GCT   379
Thr Asp Asp Asp Asp Gly Gly Pro Pro Gln Ala
            85                  90

CAC TTA GGC CGT GCC GAC CTG GTC ATG AGC TTC   412
His Leu Gly Arg Ala Asp Leu Val Met Ser Phe
        95                  100

GTC AAC ATG GTG GAA CGC GAC CGT ACC CTG GGC   445
Val Asn Met Val Glu Arg Asp Arg Thr Leu Gly
    105                 110

TAC CAG GAG CCA CAC TGG AAG GAA TTC CAC TTT   478
Tyr Gln Glu Pro His Trp Lys Glu Phe His Phe
115                 120                 125

GAC CTA ACC CAG ATC CCT GCT GGG GAG GCT GTC   511
Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val
                130                 135

ACA GCT GCT GAG TTC CGG ATC TAC AAA GAA CCC   544
Thr Ala Ala Glu Phe Arg Ile Tyr Lys Glu Pro
            140                 145
```

```
AGC ACC CAC CCG CTC AAC ACA ACC CTC CAC ATC   577
Ser Thr His Pro Leu Asn Thr Thr Leu His Ile
        150                 155

AGC ATG TTC GAA GTG GTC CAA GAG CAC TCC AAC   610
Ser Met Phe Glu Val Val Gln Glu His Ser Asn
    160                 165

AGG GAG TCT GAC TTG TTC TTT TTG GAT CTT CAG   643
Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln
170                 175                 180

ACG CTC CGA TCT GGG GAC GAG GGC TGG CTG GTG   676
Thr Leu Arg Ser Gly Asp Glu Gly Trp Leu Val
                185                 190

CTG GAC ATC ACA GCA GCC AGT GAC CGA TGG CTG   709
Leu Asp Ile Thr Ala Ala Ser Asp Arg Trp Leu
            195                 200

CTG AAC CAT CAC AAG GAC CTG GGA CTC CGC CTC   742
Leu Asn His His Lys Asp Leu Gly Leu Arg Leu
        205                 210

TAT GTG GAA ACC GCG GAT GGG CAC AGC ATG GAT   775
Tyr Val Glu Thr Ala Asp Gly His Ser Met Asp
    215                 220

CCT GGC CTG GCT GGT CTG CTT GGA CGA CAA GCA   808
Pro Gly Leu Ala Gly Leu Leu Gly Arg Gln Ala
225                 230                 235

CCA CGC TCC AGA CAG CCT TTC ATG GTA ACC TTC   841
Pro Arg Ser Arg Gln Pro Phe Met Val Thr Phe
                240                 245

TTC AGG GCC AGC CAG AGT CCT GTG CGG GCC CCT   874
Phe Arg Ala Ser Gln Ser Pro Val Arg Ala Pro
            250                 255

CGG GCA GCG AGA CCA CTG AAG AGG AGG CAG CCA   907
Arg Ala Ala Arg Pro Leu Lys Arg Arg Gln Pro
        260                 265
```

```
AAG AAA ACG AAC GAG CTT CCG CAC CCC AAC AAA   940
Lys Lys Thr Asn Glu Leu Pro His Pro Asn Lys
    270                 275

CTC CCA GGG ATC TTT GAT GAT GGC CAC GGT TCC   973
Leu Pro Gly Ile Phe Asp Asp Gly His Gly Ser
280                 285                 290

CGC GGC AGA GAG GTT TGC CGC AGG CAT GAG CTC  1006
Arg Gly Arg Glu Val Cys Arg Arg His Glu Leu
                295                 300

TAC GTC AGA TTC CGT GAC CTT GGC TGG CTG GAC  1039
Tyr Val Arg Phe Arg Asp Leu Gly Trp Leu Asp
            305                 310

TGG GTC ATC GCC CCC CAG GGC TAC TCT GCC TAT  1072
Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr
        315                 320

TAC TGT GAG GGG GAG TGT GCT TTC CCA CTG GAC  1105
Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp
    325                 330

TCC TGT ATG AAC GCC ACC AAC CAT GCC ATC TTG  1138
Ser Cys Met Asn Ala Thr Asn His Ala Ile Leu
335                 340                 345

CAG TCT CTG GTG CAC CTG ATG AAG CCA GAT GTT  1171
Gln Ser Leu Val His Leu Met Lys Pro Asp Val
                350                 355

GTC CCC AAG GCA TGC TGT GCA CCC ACC AAA CTG  1204
Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu
            360                 365

AGT GCC ACC TCT GTG CTG TAC TAT GAC AGC AGC  1237
Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser
        370                 375

AAC AAT GTC ATC CTG CGT AAA CAC CGT AAC ATG  1270
Asn Asn Val Ile Leu Arg Lys His Arg Asn Met
    380                 385
```

```
GTG GTC AAG GCC TGT GGC TGC CAC                    1294
Val Val Lys Ala Cys Gly Cys His
390                 400

TGAGGCCCCG CCCAGCATCC TGCTTCTACT ACCTTACCAT  1334
CTGGCCGGGC CCCTCTCCAG AGGCAGAAAC CCTTCTATGT  1374
TATCATAGCT CAGACAGGGG CAATGGGAGG CCCTTCACTT  1414
CCCCTGGCCA CTTCCTGCTA AAATTCTGGT CTTTCCCAGT  1454
TCCTCTGTCC TTCATGGGGT TTCGGGGCTA TCACCCCGCC  1494
CTCTCCATCC TCCTACCCCA AGCATAGACT GAATGCACAC  1534
AGCATCCCAG AGCTATGCTA ACTGAGAGGT CTGGGGTCAG  1574
CACTGAAGGC CCACATGAGG AAGACTGATC CTTGGCCATC  1614
CTCAGCCCAC AATGGCAAAT TCTGGATGGT CTAAGAAGCC  1654
CTGGAATTCT AAACTAGATG ATCTGGGCTC TCTGCACCAT  1694
TCATTGTGGC AGTTGGGACA TTTTTAGGTA TAACAGACAC  1734
ATACACTTAG ATCAATGCAT CGCTGTACTC CTTGAAATCA  1774
GAGCTAGCTT GTTAGAAAAA GAATCAGAGC CAGGTATAGC  1814
GGTGCATGTC ATTAATCCCA GCGCTAAAGA GACAGAGACA  1854
GGAGAATCTC TGTGAGTTCA AGGCCACATA GAAAGAGCCT  1894
GTCTCGGGAG CAGGAAAAAA AAAAAAAACG GAATTC      1930
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Ala Val Arg Pro Leu Arg Arg Arg Gln
 1               5
Pro Lys Lys Ser Asn Glu Leu Pro Gln
10                  15
```

Ala Asn Arg Leu Pro Gly Ile Phe Asp
20 25

Asp Val His Gly Ser His Gly Arg Gln
30 35

Val Cys Arg Arg His Glu Leu Tyr Val
40 45

Ser Phe Gln Asp Leu Gly Trp Leu Asp
50

Trp Val Ile Ala Pro Gln Gly Tyr Ser
55 60

Ala Tyr Tyr Cys Glu Gly Glu Cys Ser
65 70

Phe Pro Leu Asp Ser Cys Met Asn Ala
75 80

Thr Asn His Ala Ile Leu Gln Ser Leu
85 90

Val His Leu Met Lys Pro Asn Ala Val
95

Pro Lys Ala Cys Cys Ala Pro Thr Lys
100 105

Leu Ser Ala Thr Ser Val Leu Tyr Tyr
110 115

Asp Ser Ser Asn Asn Val Ile Leu Arg
120 125

Lys Ala Arg Asn Met Val Val Lys Ala
130 135

Cys Gly Cys His.

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1956 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Bovinae

(F) TISSUE TYPE: bone

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: human hipocampus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
GGAATTCCGG CCACAGTGGC GCCGGCAGAG CAGGAGTGGC     40
TGGAGGAGCT GTGGTTGGAG CAGGAGGTGG CACGGCAGGG     80
CTGGAGGGCT CCCTATGAGT GGCGGAGACG GCCCAGGAGG    120
CGCTGGAGCA ACAGCTCCCA CACCGCACCA AGCGGTGGCT    160
GCAGGAGCTC GCCCATCGCC CCTGCGCTGC TCGGACCGCG    200
GCCACAGCCG GACTGGCGGG TACGGCGGCG ACAGAGGCAT    240
TGGCCGAGAG TCCCAGTCCG CAGAGTAGCC CCGGCCTCGA    280
GGCGGTGGCG TCCCGGTCCT CTCCGTCCAG GAGCCAGGAC    320
AGGTGTCGCG CGGCGGGGCT CCAGGGACCG CGCCTGAGGC    360
CGGCTGCCCG CCCGTCCCGC CCCGCCCCGC CGCCCGCCGC    400
CCGCCGAGCC CAGCCTCCTT GCCGTCGGGG CGTCCCCAGG    440
CCCTGGGTCG GCCGCGGAGC CGATGCGCGC CCGCTGAGCG    480
CCCCAGCTGA GCGCCCCCGG CCTGCC ATG ACC GCG CTC   518
                             Met Thr Ala Leu
                               1

CCC GGC CCG CTC TGG CTC CTG GGC CTG GCG CTA    551
Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu
  5                  10                  15

TGC GCG CTG GGC GGG GGC GGC CCC GGC CTG CGA    584
Cys Ala Leu Gly Gly Gly Gly Pro Gly Leu Arg
                 20                  25
```

```
CCC CCG CCC GGC TGT CCC CAG CGA CGT CTG GGC   617
Pro Pro Pro Gly Cys Pro Gly arg Arg Leu Gly
            30                  35

GCG CGC GAC CGG GAC GTG CAG CGC GAG ATC CTG   650
Ala Arg Asp Arg Asp Val Gln Arg Glu Ile Leu
        40                  45

GCG GTG CTC GGG CTG CCT GGG CGG CCC CGG CCC   683
Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro
    50                  55

CGC GCG CCA CCC GCC GCC TCC CGG CTG CCC GCG   716
Arg Ala Pro Pro Ala Ala Ser Arg Leu Pro Ala
60                  65                  70

TCC GCG CCG CTC TTC ATG CTG GAC CTG TAC CAC   749
Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr His
                75                  80

CGC ATG GCC GGC GAC GAC GAC GAG GAC GGC GCC   782
Arg Met Ala Gly Asp Asp Asp Glu Asp Gly Ala
            85                  90

GCG GAG GCC CTG GGC CGC GCC GAC CTG GTC ATG   815
Ala Glu Ala Leu Gly Arg Ala Asp Leu Val Met
        95                  100

AGC TTC GTT AAC ATG GTG GAG CGA GAC CGT GCC   848
Ser Phe Val Asn Met Val Glu Arg Asp Arg Ala
    105                 110

CTG GGC CAC CAG GAG CCC CAT TGG AAG GAG TTC   881
Leu Gly His Gln Glu Pro His Trp Lys Glu Phe
115                 120                 125

CGC TTT GAC CTG ACC CAG ATC CCG GCT GGG GAG   914
Arg Phe Asp Leu Thr Gln Ile Pro Ala Gly Glu
                130                 135

GCG GTC ACA GCT GCG GAG TTC CGG ATT TAC AAG   947
Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys
            140                 145
```

```
GTG CCC AGC ATC CAC CTG CTC AAC AGG ACC CTC   980
Val Pro Ser Ile His Leu Leu Asn Arg Thr Leu
        150                 155

CAC GTC AGC ATG TTC CAG GTG GTC CAG GAG CAG  1013
His Val Ser Met Phe Gln Val Val Gln Glu Gln
    160                 165

TCC AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT  1046
Ser Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp
170                 175                 180

CTT CAG ACG CTC CGA GCT GGA GAC GAG GGC TGG  1079
Leu Gln Thr Leu Arg Ala Gly Asp Glu Gly Trp
                185                 190

CTG GTG CTG GAT GTC ACA GCA GCC AGT GAC TGC  1112
Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cys
            195                 200

TGG TTG CTG AAG CGT CAC AAG GAC CTG GGA CTC  1145
Trp Leu Leu Lys Arg His Lys Asp Leu Gly Leu
        205                 210

CGC CTC TAT GTG GAG ACT GAG GAC GGG CAC AGC  1178
Arg Leu Tyr Val Glu Thr Glu Asp Gly His Ser
    215                 220

GTG GAT CCT GGC CTG GCC GGC CTG CTG GGT CAA  1211
Val Asp Pro Gly Leu Ala Gly Leu Leu Gly Gln
225                 230                 235

CGG GCC CCA CGC TCC CAA CAG CCT TTC GTG GTC  1244
Arg Ala Pro Arg Ser Gln Gln Pro Phe Val Val
                240                 245

ACT TTC TTC AGG GCC AGT CCG AGT CCC ATC CGC  1277
Thr Phe Phe Arg Ala Ser Pro Ser Pro Ile Arg
            250                 255

ACC CCT CGG GCA GTG AGG CCA CTG AGG AGG AGG  1310
Thr Pro Arg Ala Val Arg Pro Leu Arg Arg Arg
        260                 265
```

```
CAG CCG AAG AAA AGC AAC GAG CTG CCG CAG GCC  1343
Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln Ala
    270                 275

AAC CGA CTC CCA GGG ATC TTT GAT GAC GTC CAC  1376
Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His
280                 285                 290

GGC TCC CAC GGC CGG CAG GTC TGC CGT CGG CAC  1409
Gly Ser His Gly Arg Gln Val Cys Arg Arg His
                295                 300

GAG CTC TAC GTC AGC TTC CAG GAC CTC GGC TGG  1442
Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp
            305                 310

CTG GAC TGG GTC ATC GCT CCC CAA GGC TAC TCG  1475
Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser
        315                 320

GCC TAT TAC TGT GAG GGG GAG TGC TCC TTC CCA  1508
Ala Tyr Tyr Cys Glu Gly Glu Cys Ser Phe Pro
    325                 330

CTG GAC TCC TGC ATG AAT GCC ACC AAC CAC GCC  1541
Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala
335                 340                 345

ATC CTG CAG TCC CTG GTG CAC CTG ATG AAG CCA  1574
Ile Leu Gln Ser Leu Val His Leu Met Lys Pro
                350                 355

AAC GCA GTC CCC AAG GCG TGC TGT GCA CCC ACC  1607
Asn Ala Val Pro Lys Ala Cys Cys Ala Pro Thr
            360                 365

AAG CTG AGC GCC ACC TCT GTG CTC TAC TAT GAC  1640
Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp
        370                 375

AGC AGC AAC AAC GTC ATC CTG CGC AAA GCC CGC  1673
Ser Ser Asn Asn Val Ile Leu Arg Lys Ala Arg
    380                 385
```

AAC ATG GTG GTC AAG GCC TGC GGC TGC CAC 1703
Asn Met Val Val Lys Ala Cys Gly Cys His
390 395

TGAGTCAGCC CGCCCAGCCC TACTGCAGCA ATTCACTGGC 1743
CGTCGTTTTA CAACGTGTGA CTGGGAAAAC CCTGGCGTTA 1783
CCCAACTTAA TCGCCTTGCA GCACATCCCC CTTTCGCCAG 1823
CTGGCTAATA GCGAAGAGGC CCCGCACCGA TCGCCCTTCC 1863
CAACAGTTGC GCCCCAGTGA ATGGCGAATG GCAAATTGTA 1903
AGCGTTAATA TTTTGTTAAA ATTCGCGTTA AATTTTTT 1941

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Cys Xaa_1 Xaa_2 His Glu Leu Tyr Val Xaa_3 Phe
1 5 10

Xaa_4 Asp Leu Gly Trp Xaa_5 Asp Trp Xaa_6 Ile
15 20

Ala Pro Xaa_7 Gly Tyr Xaa_8 Ala Tyr Tyr Cys
25 30

Glu Gly Cys Xaa_9 Phe Pro Leu Xaa_{10} Ser Xaa_{11}
35 40

Met Asn Ala Thr Asn His Ala Ile Xaa_{12} Thr
45 50

Leu Xaa_{13} Xaa_{14} Xaa_{15} Xaa_{16} Xaa_{17} Xaa_{18} Val
55

Pro Lys Xaa_{19} Cys Cys Ala Pro Thr Xaa_{20} Leu
60 65

Xaa_{21} Ala Xaa_{22} Ser Val Leu Tyr Xaa_{23} Asp
70 75

Xaa_{24} Ser Xaa_{25} Asn Val Xaa_{26} Leu Xaa_{27} Lys
80 85

Xaa_{28} Pro Asn Met Val Val Xaa_{29} Ala Cys Gly
90 95

Cys His,

wherein Xaa_1 = (Lys or Arg); Xaa_2 = (Lys or Arg); Xaa_3 = (Ser or Arg); Xaa_4 = (Arg or Gln); Xaa_5 = (Gln or Leu); Xaa_6 = (Ile or Val); Xaa_7 = (Glu or Gln); Xaa_8 = (Ala or Ser); Xaa_9 = (Ala or Ser); Xaa_{10} = (Asn or Asp); Xaa_{11} = (Tyr or Cys); Xaa_{12} = (Val or Leu); Xaa_{13} = (His or Asn); Xaa_{14} = (Phe or Leu); Xaa_{15} = (Ile or Met); Xaa_{16} = (Asn or Lys); Xaa_{17} = (Glu, Asp or Asn); Xaa_{18} = (Thr, Ala or Val); Xaa_{19} = (Pro or Ala); Xaa_{20} = (Gln or Lys); Xaa_{21} = (Asn or Ser); Xaa_{22} = (Ile or Thr); Xaa_{23} = (Phe or Tyr); Xaa_{24} = (Asp, Glu or Ser); Xaa_{25} = (Ser or Asn); Xaa_{26} = (Ile or Asp); Xaa_{27} = (Lys or Arg); Xaa_{28} = (Tyr, Ala or His); and Xaa_{29} = (Arg or Lys).

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 437 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Bovinae

(F) TISSUE TYPE: bone

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: human placenta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
                                                TCC ACG GGG      9
                                                Ser Thr Gly
                                                  1

AGC AAA CAG CGC AGC CAG AAC CGC TCC AAG ACG     42
Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr
      5                  10

CCC AAG AAC CAG GAA GCC CTG CGG ATG GCC AAC     75
Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn
 15                  20                  25

GTG GCA GAG AAC AGC AGC AGC GAC CAG AGG CAG    108
Val Ala Glu Asn Ser Ser Ser Asp Gln Arg Gln
                30                  35

GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC    141
Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe
            40                  45

CGA GAC CTG GGC TGG CAG GAC TGG ATC ATC GCG    174
Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala
        50                  55

CCT GAA GGC TAC GCC GCC TAC TAC TGT GAG GGG    207
Pro Glu Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly
     60                  65

GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG AAC    240
Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn
 70                  75                  80

GCC ACC AAC CAC GCC ATC GTG CAG ACG CTG GTC    273
Ala Thr Asn His Ala Ile Val Gln Thr Leu Val
                85                  90
```

```
CAC TTC ATC AAC CCG GAA ACG GTG CCC AAG CCC   306
His Phe Ile Asn Pro Glu Thr Val Pro Lys Pro
            95                  100

TGC TGT GCG CCC ACG CAG CTC AAT GCC ATC TCC   339
Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser
        105                 110

GTC CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC   372
Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
    115                 120

CTG AAG AAA TAC AGA AAC ATG GTG GTC CGG GCC   405
Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala
125                 130                 135

TGT GGC TGC CAC TAGCTCCTCC GAGAATTCAG         437
Cys Gly Cys His
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
  1               5                  10

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            15                  20

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa
        25                  30

Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
     35                  40

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
45                  50                  55
```

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
60 65

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
70 75

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
80 85

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
90 95

Xaa Cys Xaa,
100

wherein each Xaa independently represents one of the 20 naturally occurring L-isomer, α-amino acids.

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
15 20

Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
25 30

Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
45 50 55

Xaa Xaa Xaa Xaa Xaa Cys Cys Xaa Xaa Xaa Xaa
60 65

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
70 75

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
80 85

Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa,
90 95

wherein each Xaa independently represents one of the 20 naturally occurring L-isomer, α-amino acids.

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Pro Leu Arg Arg Arg Gln
1 5

Pro Lys Lys Ser Asn Glu Leu Pro Gln
10 15

Ala Asn Arg Leu Pro Gly Ile Phe Asp
20

Asp Val Asn Gly Ser His Gly Arg Gln
25 30

Val Cys Arg Arg His Glu Leu Tyr Val
35 40

Ser Phe Gln Asp Leu Gly Trp Leu Asp
45 50

Tyr Val Ile Ala Pro Gln Gly Tyr Ser
55 60

Ala Tyr Tyr Cys Glu Gly Glu Cys Ser
65

Phe Pro Leu Asp Ser Cys Met Asn Ala
70 75

Thr Asn His Ala Ile Leu Gln Ser Leu
80 85

Val His Leu Met Lys Pro Asn Ala Val
90 95

Pro Lys Ala Cys Cys Ala Pro Thr Lys
100 105

Leu Ser Ala Thr Ser Val Leu Tyr Tyr
110

Asp Glu Ser Asn Asn Val Ile Leu Arg
115 120

Lys Ala Arg Asn Met Val Val Lys Ala
125 130

Cys Gly Cys His.
135

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Arg Arg Gln
1

Pro Lys Lys Ser Asn Glu Leu Pro Gln
5 10

Ala Asn Arg Leu Pro Gly Ile Phe Asp
15 20

Asp Val Asn Gly Ser His Gly Arg Gln
25 30

Val Cys Arg Arg His Glu Leu Tyr Val
35

Ser Phe Gln Asp Leu Gly Trp Leu Asp
40 45

Tyr Val Ile Ala Pro Gln Gly Tyr Ser
50 55

Ala Tyr Tyr Cys Glu Gly Glu Cys Ser
60 65

Phe Pro Leu Asp Ser Cys Met Asn Ala
70 75

Thr Asn His Ala Ile Leu Gln Ser Leu
80

Val His Leu Met Lys Pro Asn Ala Val
85 90

Pro Lys Ala Cys Cys Ala Pro Thr Lys
95 100

Leu Ser Ala Thr Ser Val Leu Tyr Tyr
105 110

Asp Glu Ser Asn Asn Val Ile Leu Arg
115 120

Lys Ala Arg Asn Met Val Val Lys Ala
125

Cys Gly Cys His.
130

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

						Ser 1	Gln	Gln
Pro	Phe 5	Val	Val	Thr	Phe	Phe 10	Arg	Ala
Ser	Pro	Ser 15	Pro	Ile	Arg	Thr	Pro 20	Arg
Ala	Val	Arg	Pro 25	Leu	Arg	Arg	Arg	Gln 30
Pro	Lys	Lys	Ser	Asn 35	Glu	Leu	Pro	Gln
Ala 40	Asn	Arg	Leu	Pro	Gly 45	Ile	Phe	Asp
Asp	Val 50	Asn	Gly	Ser	His	Gly 55	Arg	Gln
Val	Cys	Arg 60	Arg	His	Glu	Leu	Tyr 65	Val
Ser	Phe	Gln	Asp 70	Leu	Gly	Trp	Leu	Asp 75
Tyr	Val	Ile	Ala	Pro 80	Gln	Gly	Tyr	Ser
Ala 85	Tyr	Tyr	Cys	Glu	Gly 90	Glu	Cys	Ser
Phe	Pro 95	Leu	Asp	Ser	Cys	Met 100	Asn	Ala
Thr	Asn	His 105	Ala	Ile	Leu	Gln	Ser 110	Leu
Val	His	Leu	Met 115	Lys	Pro	Asn	Ala	Val 120
Pro	Lys	Ala	Cys	Cys 125	Ala	Pro	Thr	Lys

Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
130					135			
Asp	Glu	Ser	Asn	Asn	Val	Ile	Leu	Arg
	140					145		
Lys	Ala	Arg	Asn	Met	Val	Val	Lys	Ala
		150					165	
Cys	Gly	Cys	His.					
			170					